

QY 1561 GATCGTGTGTTGAAAAAGGGGACTTGTGTTATTTGTTTCAACTTCCACTGGAGTAATAGCTA 1620
Db 1561 GATCGTGTGTTGAAAAAGGGGACTTGTGTTATTTGTTTCAACTTCCACTGGAGTAATAGCTA 1620
QY 1621 TTTCGACTACCGGGTGGCTGTTTAAAGCCTGGGAAGTACAGGTTGCTTAAAGACTCAGA 1680
Db 1621 TTTCGACTACCGGGTGGCTGTTTAAAGCCTGGGAAGTACAGGTTGCTTAAAGACTCAGA 1680
QY 1681 CGCCGACTCTTTGGGATTTGGTAGGATCCATCACACTGCAGAGCACTTCACCTTCGA 1740
Db 1681 CGCCGACTCTTTGGGATTTGGTAGGATCCATCACACTGCAGAGCACTTCACCTTCGA 1740
QY 1741 CTGCCAATGACAAACAGCCCCCATCTGTTCTCAGTGTACACTCTCTAGCAGAACCTGTGT 1800
Db 1741 CTGCCAATGACAAACAGCCCCCATCTGTTCTCAGTGTACACTCTCTAGCAGAACCTGTGT 1800
QY 1801 TGTCTATGCTCCAAATGAATTAACAGCAAGTGCAGCATACGATGCTGCTGCTCCCAAT 1860
Db 1801 TGTCTATGCTCCAAATGAATTAACAGCAAGTGCAGCATACGATGCTGCTGCTCCCAAT 1860
QY 1861 TAGCACTACAGAAAAATCTGTTGTTCAATACAAACAGGTGCAAGTTTAAATAGGGT 1920
Db 1861 TAGCACTACAGAAAAATCTGTTGTTCAATACAAACAGGTGCAAGTTTAAATAGGGT 1920
QY 1921 TTGCTTCAACGAGTCTGATAGCAAGCAACATGATGATGCTGCTGCTGCTCCCAAT 1980
Db 1921 TTGCTTCAACGAGTCTGATAGCAAGCAACATGATGATGCTGCTGCTGCTCCCAAT 1980
QY 1981 TCCAGGGCGTGTGGAGAAAAATCTCTATCTGTTATTTTATGGATCAGGGGANGAA 2040
Db 1981 TCCAGGGCGTGTGGAGAAAAATCTCTATCTGTTATTTTATGGATCAGGGGANGAA 2040
QY 2041 CTCCGCCAAACCCCTTTTGTGAAAGNGATAGGCCCGCGTNTCTGATNTG 2100
Db 2041 CTCCGCCAAACCCCTTTTGTGAAAGNGATAGGCCCGCGTNTCTGATNTG 2100
QY 2101 GATGCTCTCTAAATNTTGTAGCCATAAACCATTGCTAGTGTCTCTNTAAATGACAGTT 2160
Db 2101 GATGCTCTCTAAATNTTGTAGCCATAAACCATTGCTAGTGTCTCTNTAAATGACAGTT 2160
QY 2161 TAGAATAGNGTNTACTTTTGTATTTTNTTTTGTACAGTTAGACTGTATCTCTCAATA 2220
Db 2161 TAGAATAGNGTNTACTTTTGTATTTTNTTTTGTACAGTTAGACTGTATCTCTCAATA 2220
QY 2221 ATCGACATCTGTTTACTCGAGNTGAGAAATAAATACAGATTCAGAGTTGAGAAAAA 2280
Db 2221 ATCGACATCTGTTTACTCGAGNTGAGAAATAAATACAGATTCAGAGTTGAGAAAAA 2280
QY 2281 AAAAAAAAAAAAAAAAAAAAAA 2307
Db 2281 AAAAAAAAAAAAAAAAAAAAAA 2307

RESULT 2

ID ABK15494 standard; cDNA; 3039 BP.

XX AC ABK15494;

XX DT 08-MAY-2002 (first entry)

XX DE Wheat starch branching enzyme IIB cDNA from clone wdk2c-pk009.j17.
XX KW Wheat; starch branching enzyme; starch synthesis; transgenic plant;
XX KW wdk2c.pk009.j17; antibody; gene mapping; expressed sequence tag;
XX KW EST; gene; ss.

OS Triticum aestivum.

XX FH Key Location/Qualifiers
XX FT CDS 3..2570
XX FT /*tag= a

FT /product= "Starch branching enzyme IIB"
FT /partial
FT /note= "No start codon shown. The sequence from
FT nucleotides 481-3039 is specifically claimed in
FT claim 3 of the specification and is shown as
FT Seq ID. 1."
XX US2002002713-A1.
XX 03-JAN-2002.
XX 23-FEB-2001; 2001US-0792127.
XX 01-MAR-2000; 2000US-186098P.
XX (ALLE/) ALLEN S M.
XX (BECK/) BECKLES D M.
XX (BUTL/) BUTLER K H.
XX (PEAR/) PEARLSTEIN R W.
XX Allen SM, Beckles DM, Butler KH, Pearlstein RW;
XX WPI; 2002-178959/23.
XX P-PSDB; AAU76219.

Novel isolated polypeptide having starch IIB enzyme activity, useful for preparing antibodies to the proteins which are used to detect the polypeptides in situ in cells or in vitro in cell extracts

Claim 3; Page 17-18; 27pp; English.

This invention relates to the cDNA and protein sequences of a novel wheat starch branching enzyme IIB enzyme. Starch branching enzymes are responsible for the formation of alpha 1-6 linkages in amylopectin in the starch synthesis pathway. The nucleotide sequence of the invention is useful for producing a transgenic plant expressing the starch branching enzyme. The protein sequence is useful for preparing antibodies against starch branching enzyme IIB protein, which are useful for detecting the proteins in situ in cells, or in vitro in cell extracts. The protein is also useful for selecting an isolated polynucleotide that affects the level of expression of a starch branching enzyme IIB protein or enzyme activity in a plant cell. All or substantial portion of the nucleotide sequence can be used as probe for genetic and physical mapping of the genes and can be used as markers for traits linked to those genes. This information is useful in plant breeding in order to develop lines with desired phenotypes. A polynucleotide fragment is useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species. They are also useful as DNA hybridisation probes or as polymerase chain reaction (PCR) amplification primers. The fragments are also useful for creating transgenic plants and may be useful as restriction fragment length polymorphism markers. Nucleic acid probes derived from the cDNA sequence may also be used for physical mapping or for fluorescence in situ hybridisation (FISH) mapping. The present sequence represents the wheat starch branching enzyme IIB cDNA from clone wdk2c.pk009.j17.

Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 other;

Query Match 91.8% Score 2118.4; DB 24; Length 3039;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 54; Indels 8; Gaps 4;

QY 45 TTGGTGTCTGGGAGATGTTCTTGGCAACAATGAGATGGTTCGCCACCAATTCCTCAG 104
Db 793 TTGGTGTCTGGGAGATGTTCTTGGCAACAATGAGATGGTTCGCCACCAATTCCTCAG 852
QY 105 GCTACCGGTGAAGTGAAGATGGATCTCCATCTGGGATAAAGGATTCATTCCTGCTT 164
Db 853 GCTACCGGTGAAGTGAAGATGGATCTCCATCTGGGATAAAGGATTCATTCCTGCTT 912
QY 165 GSATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATCAATGAATATATTATGATC 224
Db 913 GSATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATCAATGAATATATTATGATC 972

QY 225 CTCCGAGAGAGAGTATGTTTCAAGCATCTCAACCTAACACCAAAATCATTCG 284
 Db 973 CTCCGAGAGAGAGATGTTTCAAGCATCTCAACCTAACACCAAAATCATTCG 1032
 QY 285 GGATATATGAACACATGTTGGCATGAGTAGCCCGGAACAAAGATCAACACATATGCAA 344
 Db 1033 GGATATATGAACACATGTTGGCATGAGTAGCCCGGAACAAAGATCAACACATATGCAA 1092
 QY 345 ACTTCAGGATGAGTCTTCCAGAAATTAAGAGCTTGGATACAAATGAGTGCATAATAA 404
 Db 1093 ACTTCAGGATGAGTCTTCCAGAAATTAAGAGCTTGGATACAAATGAGTGCATAATAA 1152
 QY 405 TGGCAATCCAGGAGCACTCATATGTAAGAGCTTGGGATACCATGTTTCCAAATCTCTTGG 464
 Db 1153 TGGCAATCCAGGAGCACTCATATGTAAGAGCTTGGGATACCATGTTTCCAAATCTCTTGG 1212
 QY 465 CACCAAGTAGCCGTTTGGGTCGCCAGAGATTTAAATCTTTGATGATAGAGCTCAGG 524
 Db 1213 CACCAAGTAGCCGTTTGGGTCGCCAGAGATTTAAATCTTTGATGATAGAGCTCAGG 1272
 QY 525 AGCTTGGCTTGGTTCCTCATGGATGTTGTTACAGAGTCAAGGTCACAAATATACCTTGG 584
 Db 1273 AGCTTGGCTTGGTTCCTCATGGATGTTGTTACAGAGTCAAGGTCACAAATATACCTTGG 1332
 QY 585 ACGGGTTGAATGGTTTGGATGGCAGCATACACATTTACATGCGGTTTCCAGGGGCC 644
 Db 1333 ACGGGTTGAATGGTTTGGATGGCAGCATACACATTTACATGCGGTTTCCAGGGGCC 1392
 QY 645 ATCACTGGATGGGATTCCTGTTGTTAACTATGGGAATAAGGAAGTTATAAGGTTTC 704
 Db 1393 ATCACTGGATGGGATTCCTGTTGTTAACTATGGGAATAAGGAAGTTATAAGGTTTC 1452
 QY 705 TACTTTCCATGCAAGATGGTGCAGAGATTAAGTTGATGTTTCCGATTCGATG 764
 Db 1453 TACTTTCCATGCAAGATGGTGCAGAGATTAAGTTGATGTTTCCGATTCGATG 1512
 QY 765 GCGGACCTCCATGATATACCATCATGATTTACAGTAACCTTTACAGGAAGCTACC 824
 Db 1513 GCGGACCTCCATGATATACCATCATGATTTACAGTAACCTTTACAGGAAGCTACC 1572
 QY 825 ATGAATATTTTGGCTTGGCATGATGATGCGGTGCTTTTACTGTGATGATGAATG 884
 Db 1573 ATGAATATTTTGGCTTGGCATGATGATGCGGTGCTTTTACTGTGATGATGAATG 1632
 QY 885 ATCTAATTCATGGTTTATCTGAAGCGGTAACTATCGGTGAAGATGTTAGTGAATGC 944
 Db 1633 ATCTAATTCATGGTTTATCTGAAGCGGTAACTATCGGTGAAGATGTTAGTGAATGC 1692
 Y 945 CTACATTTGCCCTTCTGTTCAAGTTGGTGGGTTGGTTTGGATATCGCTTACATATGG 1004
 Db 1693 CTACATTTGCCCTTCTGTTCAAGTTGGTGGGTTGGTTTGGATATCGCTTACATATGG 1752
 QY 1005 CTGTTGCCACAAATGGATGATCTCAAGGAAACGATGAAGCTTGGGAGATGGGTA 1064
 Db 1753 CTGTTGCCACAAATGGATGATCTCAAGGAAACGATGAAGCTTGGGAGATGGGTA 1812
 QY 1065 ATATTGTGCACACACTAACAAACAGAGGTGGCCGGAAGGTGCTTACTTATGCTGAAA 1124
 Db 1813 ATATTGTGCACACACTAACAAACAGAGGTGGCTGGAAGGTGCTTACTTATGCTGAAA 1872
 QY 1125 GTCACGATCAAGCACTGGTTGGAGACAGACTTATTCATTTCTGTTGATGGACAAAGGATA 1184
 Db 1873 GTCACGATCAAGCACTGGTTGGAGACAGACTTATTCATTTCTGTTGATGGACAAAGGATA 1932
 QY 1185 TGTATGATTTTCACTGCTGAAGCGACCTTCCACACCTAGTATTTGATCGTGAATAGCAC 1244
 Db 1933 TGTATGATTTTCACTGCTGAAGCGACCTTCCACACCTAGTATTTGATCGTGAATAGCAC 1992
 QY 1245 TGCATAAAATGATAGACTTATCAAAATGGGTTTAGGAGGAGAGGTTTATCTTAACTTTA 1304
 1993 TGCATAAAATGATAGACTTATCAAAATGGGTTTAGGAGGAGAGGTTTATCTTAACTTTA 2052

QY 1305 TGGGAATGAGTTTGGGCATCTCAATGGATAGACTTTCCAGAGAGGCCACAGTACTTC 1364
 Db 2053 TGGGAATGAGTTTGGGCATCTCAATGGATAGACTTTCCAGAGAGGCCACAGTACTTC 2112
 QY 1365 CAACCTGGTAACTTCCAGGAAACAAACACAGTTAGCAAAATGCCGTCGAAGATTG 1424
 Db 2113 CAAGTGGTAACTTCCAGGAAACAAACACAGTTAGCAAAATGCCGTCGAAGATTG 2172
 QY 1425 ACCAGGATGATGCAAGATTTCTTAGGTATCATGGTATGCAGCAGTTTGTATCAGGCGATGC 1484
 Db 2173 ACCTGGGATGATGCAAGATTTCTTAGGTATCATGGTATGCAGCAGTTTGTATCAGGCGATGC 2232
 QY 1485 AGCATCTGAGGAAATATGGCTTTATGACATCAGACACCACTAGTATCTCGGAAC 1544
 Db 2233 AGCATCTGAGGAAATATGGCTTTATGACATCAGACACCACTAGTATCTCGGAAC 2292
 QY 1545 ATGAGGAAGATAAGGTGATCGTGTGTTGAAAAGGGGACTTGGTATTTGTTCAACTTCC 1604
 Db 2293 ATGAGGAAGATAAGGTGATCGTGTGTTGAAAAGGGGACTTGGTATTTGTTCAACTTCC 2352
 QY 1605 ACTGGAGTAAATAGCTATTTGACTACCGGGTGGCTGTTTAAAGCCTGGGAAGTACAAG 1664
 Db 2353 ACTGGAGTAAATAGCTATTTGACTACCGGGTGGCTGTTTAAAGCCTGGGAAGTACAAG 2412
 QY 1665 TTGCTTTAGACTCAGACGCGGACTCTTGGTGGATTTGGTAGGATCCATCAGCAGTCCAG 1724
 Db 2413 TTGCTTTAGACTCAGACGCGGACTCTTGGTGGATTTGGTAGGATCCATCAGCAGTCCAG 2472
 QY 1725 AGCACTTCACTTCTGACTGCAACATGACACAGGCCCCCTTCTCAGTGTACACTC 1784
 Db 2473 AGCACTTCACTTCTGACTGCAACATGACACAGGCCCCCTTCTCAGTGTACACTC 2532
 QY 1785 CTAGCAGAACTGTGTTGCTATGCTCCATGAATGAACAAAGAGTGCAGCATAGCA 1844
 Db 2533 CTAGCAGAACTGTGTTGCTATGCTCCATGAATGAACAAAGAGTGCAGCATAGCG 2591
 QY 1845 TGCACGCTGTTGTTGCTAGCACTAGCAAGAAATGCTATGTTCAATCAACACAGTGC 1904
 Db 2592 TGCACGCTGTTGTTGCTAGCACTAGCAAGAAATGCTATGTTCAATCAACACAGTGC 2647
 QY 1905 AAGTTTAAATAAGG - -GTTTGTTCACAGAGTCTCTGATAGCAAGCAACATGATGATG 1962
 Db 2648 AAGTTTAAATAAGGATTTTGTCTCAACAGAGTCTCTGATAGCAAGCAACATGATGATG 2707
 QY 1963 TGCTCTGCTCCCAATTCGAGGCGTGTGAGGAGAAATGCTCATCTGTTGTTATTT 2022
 Db 2708 TGCTCTGCTCCCAATTCGAGGCGTGTGAGGAGAAATGCTCATCTGTTGTTATTT 2766
 QY 2023 TATGGATCAGGAGAAACCTCCGCCAAANACCCCTTTTGTGAAAGGNGGATAGGC 2082
 Db 2767 TATGGATCAGGAGAAACCTCCGCCAAANACCCCTTTTGTGAAAGGNGGATAGGC 2826
 QY 2083 CCGCGTNTCTGATNTGGATGCTCTCTTAAATNTTGTAGCCATTAACCATTCGTAGTG 2142
 Db 2827 CCGCGTNTCTGATNTGGATGCTCTCTTAAATNTTGTAGCCATTAACCATTCGTAGTG 2886
 QY 2143 TCCTNTAAATGACAGTTTAAAGATAGGTTTACTTGTATTTTGTGACAGTTA 2202
 Db 2887 TCCTNTAAATGACAGTTTAAAGATAGGTTTACTTGTATTTTGTGACAGTTA 2946
 QY 2203 GACTGTATTCCTCAAAATATCGACATGTTGTTTACTCGAAGTGAAGATAAATAACAGAG 2262
 Db 2947 GACTGTATTCCTCAAAATATCGACATGTTGTTTACTCGAAGTGAAGATAAATAACAGAG 3006
 QY 2263 ATTGNAGNAAAAAAGGAAAAAAGGAAAAA 2295
 Db 3007 ATTGAAGATTCACAAAAAAGGAAAAAAGGAAAAA 3039

RESULT 3
 AAH78342
 ID AAH78342 standard; cDNA; 2968 BP.
 XX

DR Pfam: PF02922; isoamylase_N: 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 823 AA; 92970 MW; 5891580B665A462A CRC64;
 Query Match 70.2%; Score 2900; DB 10; Length 823;
 Best Local Similarity 87.1%; Pred. No. 4.5e-223;
 Matches 513; Conservative 45; Mismatches 31; Indels 0; Gaps 0;

QY 14 FGWEMFLPNADSPPIPHGSRVYKVRMDTPSGIKDSIPAWIKYSVQTPGDIPYNGIYD 73
 DB 232 YGWEIFLPNADSPPIPHGSRVYKVRMDTPSGIKDSIPAWIKYSVQTPGDIPYNGIYD 291

QY 74 PPEEKYVFKHPKPKSLRIYETHVGMSSPEPKINTYANFRDEVLPRIKRLGYNVQI 133
 DB 292 PPEEKYVFKHPKPKSLRIYETHVGMSSPEPKINTYANFRDEVLPRIKRLGYNVQI 351

QY 134 MAIQEHSYASFGYHYTNFAPSSRFGSPEDLSLIDRAHELGLVLMVDSHSSNNTL 193
 DB 352 MAIQEHSYASFGYHYTNFAPSSRFGSPEDLSLIDRAHELGLVLMVDSHSSNNTL 411

QY 194 DGLNGFDGTDTHYFHGGSRGHMMDSRVFNNGKVEIRFLLSNARWLEEKYKDGFRFD 253
 DB 412 DGLNGFDGTDTHYFHGGSRGHMMDSRVFNNGKVEIRFLLSNARWLEEKYKDGFRFD 471

QY 254 GATSMYTHHGLQVTFGYSHEYEGFATDVAVYLMNDLHGLHPDAVSGEDVSGM 313
 DB 472 GATSMYTHHGLQVTFGYSHEYEGFATDVAVYLMNDLHGLHPDAVSGEDVSGM 531

QY 314 PTFALPVGVGVGDFYRLHMAVADKWIELLKGNDEAWEMGNIVHTLTNRWRPERKCVYAE 373
 DB 532 PTFALPVGVGVGDFYRLHMAVADKWIELLKGNDEAWEMGNIVHTLTNRWRPERKCVYAE 591

QY 374 SHDQALVGDKTIAFWLMDKMDYDFMALNGPSTPRIDRGIALHKMIRLITMGLGEGYLN 433
 DB 592 SHDQALVGDKTIAFWLMDKMDYDFMALNGPSTPRIDRGIALHKMIRLITMGLGEGYLN 651

QY 434 MGNEFGHEPWIDPRGPQVLTGKFIPIGNNSYDKCRRRFDGDAEFLRYHGMQEQDAM 493
 DB 652 MGNEFGHEPWIDPRGPQVLTGKFIPIGNNSYDKCRRRFDGDAEFLRYHGMQEQDAM 711

QY 494 OHLEEKYGMTSDHQYVSRKHEEDKVIIFERGLDVFVFNFWNSYFYDYRVGCKLPKQYK 553
 DB 712 OHLEEKYGMTSDHQYVSRKHEEDKVIIFERGLDVFVFNFWNSYFYDYRVGCKLPKQYK 771

QY 554 VVLDSAGLFGGFGRIHHTAEHTSDCOHNRPHSFVSFVTPSRCTCVVYA 602
 DB 772 VALDSDALFGGFGRLDHDVDYFTTEHPHNDNRPSFSVYTPSRCTCVVYA 820

RESULT 8
 P93691
 ID P93691 PRELIMINARY; PRT: 823 AA.
 AC P93691;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 1.4-alpha-glucan branching enzyme II precursor (EC 2.4.1.18).
 GN SBE2.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, FIELDER;
 RA Nair R.B., Baga M., Scoles G.J., Kartha K.K., Chibbar R.N.;
 RT "Isolation, characterization and expression analysis of a starch
 branching enzyme II cDNA from wheat."
 RL Plant Sci. 0:0-0(0).
 DR EMBL: Y11282; CAA72154.1;
 DR InterPro: IPR000461; Alpha.amylase.
 DR InterPro: IPR004193; Isoamylase_N.

DR Pfam: PF00128; alpha-amylase; 1.
 KW Glycosyltransferase; Signal; Transferase.
 FT SIGNAL 1 54
 FT CHAIN 55 823
 SQ SEQUENCE 823 AA; 92935 MW; 80135FA52CBA4549 CRC64;
 Query Match 70.1%; Score 2894; DB 10; Length 823;
 Best Local Similarity 86.9%; Pred. No. 1.4e-222;
 Matches 512; Conservative 45; Mismatches 32; Indels 0; Gaps 0;

QY 14 FGWEMFLPNADSPPIPHGSRVYKVRMDTPSGIKDSIPAWIKYSVQTPGDIPYNGIYD 73
 DB 232 YGWEIFLPNADSPPIPHGSRVYKVRMDTPSGIKDSIPAWIKYSVQTPGDIPYNGIYD 291

QY 74 PPEEKYVFKHPKPKSLRIYETHVGMSSPEPKINTYANFRDEVLPRIKRLGYNVQI 133
 DB 292 PPEEKYVFKHPKPKSLRIYETHVGMSSPEPKINTYANFRDEVLPRIKRLGYNVQI 351

QY 134 MAIQEHSYASFGYHYTNFAPSSRFGSPEDLSLIDRAHELGLVLMVDSHSSNNTL 193
 DB 352 MAIQEHSYASFGYHYTNFAPSSRFGSPEDLSLIDRAHELGLVLMVDSHSSNNTL 411

QY 194 DGLNGFDGTDTHYFHGGSRGHMMDSRVFNNGKVEIRFLLSNARWLEEKYKDGFRFD 253
 DB 412 DGLNGFDGTDTHYFHGGSRGHMMDSRVFNNGKVEIRFLLSNARWLEEKYKDGFRFD 471

QY 254 GATSMYTHHGLQVTFGYSHEYEGFATDVAVYLMNDLHGLHPDAVSGEDVSGM 313
 DB 472 GATSMYTHHGLQVTFGYSHEYEGFATDVAVYLMNDLHGLHPDAVSGEDVSGM 531

QY 314 PTFALPVGVGVGDFYRLHMAVADKWIELLKGNDEAWEMGNIVHTLTNRWRPERKCVYAE 373
 DB 532 PTFALPVGVGVGDFYRLHMAVADKWIELLKGNDEAWEMGNIVHTLTNRWRPERKCVYAE 591

QY 374 SHDQALVGDKTIAFWLMDKMDYDFMALNGPSTPRIDRGIALHKMIRLITMGLGEGYLN 433
 DB 592 SHDQALVGDKTIAFWLMDKMDYDFMALNGPSTPRIDRGIALHKMIRLITMGLGEGYLN 651

QY 434 MGNEFGHEPWIDPRGPQVLTGKFIPIGNNSYDKCRRRFDGDAEFLRYHGMQEQDAM 493
 DB 652 MGNEFGHEPWIDPRGPQVLTGKFIPIGNNSYDKCRRRFDGDAEFLRYHGMQEQDAM 711

QY 494 OHLEEKYGMTSDHQYVSRKHEEDKVIIFERGLDVFVFNFWNSYFYDYRVGCKLPKQYK 553
 DB 712 OHLEEKYGMTSDHQYVSRKHEEDKVIIFERGLDVFVFNFWNSYFYDYRVGCKLPKQYK 771

QY 554 VVLDSAGLFGGFGRIHHTAEHTSDCOHNRPHSFVSFVTPSRCTCVVYA 602
 DB 772 VALDSDALFGGFGRLDHDVDYFTTEHPHNDNRPSFSVYTPSRCTCVVYA 820

RESULT 9
 Q9ZTB7
 ID Q9ZTB7 PRELIMINARY; PRT: 734 AA.
 AC Q9ZTB7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DE 1.4-alpha-glucan branching enzyme IIA (EC 2.4.1.18).
 GN SBE1 OR SBE1A.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, BOMI;
 RX MEDLINE=98404232; PubMed=9733524;
 RA Sun C., Sathish P., Ahlstrandberg S., Jansson C.;
 RT "The two genes encoding starch-branching enzymes IIA and IIB are
 differentially expressed in barley."

Db 2392 GAGCACTTCACCGCGGACTGTTGGCATGATAATAGGCCATATTCATTCGCGTTTATACA 2451
Qy 1784 CCTAGCAGAACCTGTGTGCTATGCTCCCAATGAACATA 1822
Db 2452 CCAGCAGACATGTGCTGTATGCTCCAGTGGAGTGA 2490

RESULT 7

AAT69729

ID AAT69729 standard; DNA; 2665 BP.

XX AC AAT69729;

XX DT 10-SEP-1997 (first entry)

XX Plasmid pBE240 insert encoding corn starch branching enzyme IIB.

XX Starch branching enzyme IIB; SBEIIB; corn; maize; antisense;

XX amylopectin; transgenic plant; pBE240; ss.

XX OS Zea mays.

XX Key Location/Qualifiers

XX CDS 79..2478

XX /*tag= a

XX W09722703-A2.

XX 26-JUN-1997.

XX 12-DEC-1996; 96W0-US19678.

XX 20-DEC-1995; 95US-0009113.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Broglie KE, Hubbard NL, Klein TM;

XX WPI; 1997-341694/31.

XX P-PSDB; AAW19212.

Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff

Example 1; Page 50-53; 92pp; English.

A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI-XhoI fragment isolated from a corn cDNA library. It includes an open reading frame encoding starch branching enzyme IIB (SBEIIB) (AAW19212). The insert was used as a starting point in the assembly of DNA constructs (see also AAT69730, AAT69736-37) designed to achieve suppression of SBEIIB expression in transgenic corn plants, and thereby to produce novel starches that have properties beneficial in food and industrial applications.

Sequence 2665 BP; 700 A: 525 C; 705 G; 735 T; 0 other;

Query Match 59.8%; Score 1380.6; DB 18; Length 2665;
Best Local Similarity 86.0%; Pred. No. 9.2e-305;
Matches 1530; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

Qy 44 TTTCGTGTGGGAGATGTTCTTCCAAACATGACAGATGTTCCGCCACCAATTCCTCAC 103

Db 700 TTTCGTGTGGGAAATTTTCTGCTTACATGACAGATGTTACATTCCTCAT 759

Qy 104 GGCTCAGCGTGAAGTGAAGATGAGATCTCCATCTGGGATAAAGATTCATTCCTCT 163

Db 760 GGATCTCGTGAAGTGAAGATGAGATCTCCATCTGGGATAAAGATTCATTCACGCC 819

164 TGGATCAAGTACTCCGTCGAGATCTCCAGGAGATATACCATATATATATAT 223

Db 820 TGGATCAAGTACTCAGTCAGGCCCGCCAGGAAATACCATATGATGGATTATTATGAT 879
Qy 224 CCTCCGGAAGAGAGATGATGTTTCAAGCATCCTCAACCTAAACCCAAATCATG 283
Db 880 CTTCTTGAAGAGTAAAGTGTGTTCAGGCATGCGCAACCTAAACCCAAATCATG 939
Qy 284 CGGATATATGAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAACACATATGTA 999
Db 344 AACTTCAGGATGAGTGTCTCCAGAAATTAAGACATGATCAATGAGTCAGTCAATA 403
Db 1000 AACTTTAGGATGAAGTCTCCCAAGAATAAAACACTTTGGATACATGAGTCAGTCAATA 1059
Qy 404 ATGCCAATCCAGGAGCACTCATCTATGGAAGCTTTGGGTACCATGTTTACCAATCTTT 463
Db 1060 ATGGCAATCCAGGAGCACTCATCTATGGAAGCTTTGGATACCATGTAACATTAATTTT 1119
Qy 464 GCACCAAGTAGCCGTTTGGGTCCCAAGATTTAAATCTTTTGGATGATAGAGTCAC 523
Db 1120 GCGCCAAAGTAGTCGTTTGGTACCCAGAGATTTGAAGTCTTTGGATGATAGAGCACAT 1179
Qy 524 GAGCTTGGCTTGGTGTCTCATGATGTTTGTTCACAGTCACGCGTCAAAATAATACCTTG 583
Db 1180 GAGCTTGGTGTCTCATGATGTTTGTTCACAGTCACGCGTCAAAATAATACCTTG 1239
Qy 584 GAGGGTTGAATGGTTTGGTGGGACGATACACATTTACCTTCCATGGCGTTACGGGGC 643
Db 1240 GATGGTTGAATGGTTTGGTGGGACGATACACATTTACCTTCCATGGCGTTACGGGGC 1299
Qy 644 CATCACTGATGTTGGGATTCCTCGTGTGTTTAACTATGGGAATAAGGAAGTTTAAAGTTT 703
Db 1300 CATCACTGATGTTGGGATTCCTCGTGTGTTTAACTATGGGAATAAGGAAGTTTAAAGTTT 1359
Qy 704 CTACTTCCAAATGCAAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 763
Db 1360 CTCTCTCCAAATGCTAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1419
Qy 764 GCGCGACCTCCATGATGATATACCATCATGATGATGATGATGATGATGATGATGATGATG 823
Db 1420 GGTGTGACCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1479
Qy 824 CATGATATTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 883
Db 1480 AATGAGTATTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1539
Qy 884 GATCTAATTCATGGGTTTATCTCTGAAGCCCTTAACCTATCGTGAAGATGTTAGTGGAAATG 943
Db 1540 GATCTAATTCATGGGTTTATCTCTGAAGCCCTTAACCTATCGTGAAGATGTTAGTGGAAATG 1599
Qy 944 CCTACATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1003
Db 1600 CCTACATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1659
Qy 1004 GCTGTTCGCGCAAAATGGAATGAACTTCTCAAGGAACAGATGAAGCTTGGGAGATGGGT 1063
Db 1660 GCTGTTCGCGCAAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1719
Qy 1064 AATATGTCACACACTAACAACAGAGAGTGGCGGAGAAAGTGTGTGTGTGTGTGTGTGTGT 1123
Db 1720 GATATGTCACACACTAACAACAGAGAGTGGCGGAGAAAGTGTGTGTGTGTGTGTGTGTGT 1779
Qy 1124 AGTCAGATCAAGCACTGGTGGACAAAGACTATTGCTTCTGTTGATGGACAAAGAT 1183
Db 1780 AGTCAGATCAAGCACTGGTGGACAAAGACTATTGCTTCTGTTGATGGACAAAGAT 1839
Qy 1184 ATGTATGATTCATGGCTGTGAACGGACCTTCGACACCTAGTATGATGATGATGATGATGATG 1243
Db 1840 ATGTATGATTCATGGCTGTGAACGGACCTTCGACACCTAGTATGATGATGATGATGATGATG 1899
Qy 1244 CTGCATAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
Db 1900 TTACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1959

DR P-PSDB; AAW41763.
XX
PT Rice starch branching enzyme gene - synthesises amylopectin to yield
PT high quality starch
XX
XX Claim 4; pages 5-8; 13pp; Japanese.
XX
XX The present sequence encodes the rice type IV starch branching
CC enzyme, which has the ability to synthesise amylopectin. The
CC quality of starch is improved by the use of the protein.
XX
SQ Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;

Query Match	56.8%;	Score 1310.4;	DB 19;	Length 3015;
Best Local Similarity	83.8%;	Pred. No. 9.5e-289;		
Matches 1482;	Conservative 0;	Mismatches 286;	Indels 0;	Gaps
QY	44	TTTGTGTGTGGAGATGTTCTTGCACAAACATCGAGATGGTTCGCCACCAATTCCTTCAC	103	
Db	873	TTTGTGTGTGGAGATTCCTCGCTCAACATGCTGATGATGCCCTGCTATTCCCTCAT	932	
QY	104	GGCTCACGGGTGAAGTGGAGATGATCTCCATCTGGGATAAAGGATTCAATTCCCTGCT	163	
Db	933	GGCTCACGTGTAAGATTCGGATGGATACACACCTCGCGTAAAGGATTCAAATTCCTGCC	992	
QY	164	TGGATCAAGTACTCCGTGCAGACTCCAGAGATATACCATACAATGGAATATATATGAT	223	
Db	993	TGGATTAAAGTTGCTGTGCAGGCTCCAGGTGAATATACCGTACAACGGTATATATATGAT	1052	
QY	224	CTCCCGAAGGAGGAAGTATGTATTCAAGCATCCTCAACCTAAACGACCAAAATCATTG	283	
Db	1053	CCACTGGAAGAANAATATGTATTCCACATCCTCAACCTAAACGACCAAAATTCGCTG	1112	
QY	284	CGGATATATGAACACATGTTGGCATGATAGCCGGCAACCAAAAGATCAACACATATGCA	343	
Db	1113	CGGATATATGAATACATATATGGATGATAGCCCGGACCGAAGATTAACACATATGCT	1172	
QY	344	AAC TTCAGGATGAGGTGCTTCCAAAGAAATTAAGACATTGGATACAATGCAGTCAAAATA	403	
Db	1173	AATTTTAGGGATGAGGTGCTACCAAGAAATTAAGAAAGCTTGGGTACAATGCTGTACAGATA	1232	
QY	404	ATGGCAATCCAGGACACTATACTATGGAAGCTTTCGGTACCATGTTACCAATTTCTTT	463	
Db	1233	ATGGCAATCCAGGACACTTTATTACGAAGCTTGGGTATCATGTTACTAACTTCCTTT	1292	
QY	464	GCACCAAGTAGCCGTTTGGGTCCCCAGAAATTTAAATCTTTGATTGATAGAGCTCAC	523	
Db	1293	GGCCCAAGTAGCCGTTTCGGAACCCAGAAAGACTTGAATCTCTGATGATAAGCTCAC	1352	
QY	524	GAGCTTGGCTTGGTTGCTCATGGATGTTGTTCCACAGTCACGCGTCAAAATAATACCTTG	583	
Db	1353	GAGCTTGGTTTGGCTTGTACTTATGGATATGTTCCACAGTCATGATCAAAACAATACCTTG	1412	
QY	584	GACGGTGTGAATGTTTGTATGGCAGGATACACATTACTTCCATGCGGTTTCACGGGGC	643	
Db	1413	GATGGTTTGAATGTTTGTATGGTACTGATACACATTACTTCCATGCTGTCACACCGGGT	1472	
QY	644	CATCACTGGATGTGGGATTCOCGCTGTTTAACTATCGGAATAGGAAGTTATAAGTGT	703	
Db	1473	CATCACTGGATGTGGGATTCGCGCTGTTTCAACTATGGGAGTTGGGAAGTTTAAAGATAT	1532	
QY	704	CTACTTCCAAATGCAAGATGGTGGCTAGAGAGATATAAGTTTGATGTTTCCGATTCGAT	763	
Db	1533	TTACTGTGCAATGCAAGTGGTGGCTTGAAGATACAAAGTTTGAATGGTTTCCATTTGAT	1592	
QY	764	GGCGGACCTCCATGATGTATACCCATCATGGAATACAAGTAACCTTTACAGGAAGCTAC	823	
Db	1593	GGGTGACCTCCATGATGTATCTCATCATGTTTACAGTGGCATTTACTGCGCAACTAT	1652	
QY	824	CATCAATATTTTGGCTTTCACATGATAGTAGCGGTGCTTTTACTTGATGCTGATGAAT	883	
Db	1653	GGCGAATATTTTGGATTTGCTAGTATGTTGATGCAAGTACTTTACTTGATGCTGGTGAAC	1712	

RESULT 8	
AAV05639	
ID	AAV05639 standard; cDNA to mRNA; 3015 BP.
XX	
XX	AAV05639;
XX	
XX	01-MAY-1998 (first entry)
XX	
DE	Rice type IV starch branching enzyme cDNA.
XX	
XX	Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX	
OS	Oryza sativa.
XX	
XX	Key
FF	Location/Qualifiers
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FT	/*tag= b
FT	288..2651
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XX	JPI0004970-A.
PPD	13-JAN-1998.
XX	
PPF	24-JUN-1996; 96JP-0162983.
XX	
PPR	24-JUN-1996; 96JP-0162983.
XX	
XX	(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA	(MITK) MITSUI TOATSU CHEN INC.
XX	
XX	WPI: 1998-133625/13.

QY 464 GCACCAAGTAGCGGTTTGGTCCCGCAGAGATTTAAATCTTTGATTGATAGAGCTCAC 523
Db 1264 GCACCAAGTAGCGGTTTGGTCCCGCAGAGATTTAAATCTTTGATTGATAGAGCTCAC 1323
QY 524 GAGCTTGGCTTGGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 583
Db 1324 GAGCTTGGCTTGGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1383
QY 584 GAGCGGTGGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 643
Db 1384 GAGCGGTGGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1443
QY 644 CATCAGTGGATGGGATTCCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 703
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QY 704 CTACTTTCCCAATCAGAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 763
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QY 764 GGCAGACCTCCATGATGATATCCCATCATGATGATGATGATGATGATGATGATGATGATG 823
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QY 1064 AATATTGTCACACACTAACAAACAGAGAGTGGCGGAAAGTGTACTTATGCTGAA 1123
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QY 1124 AGTCATGATCAAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1183
Db 1924 AGTCATGATCAAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1983
QY 1184 ATGTATGATTCATGCTCTGACGGACCTTCGACACCTAGTATGATGATGATGATGATGATG 1243
Db 1984 ATGTATGATTCATGCTCTGACGGACCTTCGACACCTAGTATGATGATGATGATGATGATG 2043
QY 1244 CTGCATAAATGATTACACTTATCACAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1303
Db 2044 CTGCATAAATGATTACACTTATCACAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2103
QY 1304 ATGGGAATGAGTTCGGGATCCTGGAATGAGTATGATGATGATGATGATGATGATGATGATG 1363
Db 2104 ATGGGAATGAGTTCGGGATCCTGGAATGAGTATGATGATGATGATGATGATGATGATGATG 2163
QY 1364 CCAACTGGTATGATTCAGGAGAAACAAACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1423
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Db 2224 GACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2283
QY 1484 CAGCATCTTGGAGAAAATATGGCTTTTATGATGATGATGATGATGATGATGATGATGATG 1543
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QY 1544 CATGAGGAAGATAAGGTGATGCTGTTGTTGAAAAGGGGACTTGGTATTTGTTGTTCAACTTC 1603

Db 2344 CATGAGGAAGATAAGGTGATCATCTTCGAAAAGAGAGATTGGTATTTGTTTCAACTTC 2403
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RESULT 12
AF064560
LOCUS
DEFINITION
Hordeum vulgare cultivar Bomi starch branching enzyme Ila (sbeIIa)
mRNA, nuclear gene encoding plastid protein, complete cds.
ACCESSION
AF064560
VERSION
AF064560.1 GI:3822019
KEYWORDS
Hordeum vulgare subsp. vulgare.
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 2554)
Sun, C., Sathish, P., Ahlensberg, S. and Jansson, C.
The two genes encoding starch-branching enzymes Ila and I Ib are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
JOURNAL
MEDLINE
98404232
PUBMED
9733524
REFERENCE
2 (bases 1 to 2554)
Sun, C., Sathish, P., Ahlensberg, S. and Jansson, C.
Direct Submission
Submitted (11-MAY-1998) Stockholm University, Biochemistry,
Stockholm S-10691, Sweden
FEATURES
Location/Qualifiers
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DGVGFYRLHMAVDKWIELLKQSDSRWKGDIIVTLNRRLWEKCVTAESDQAL
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